

GenCore version 5.1.6  
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# DM nucleic - nucleic search, using sw model

Run on: December 3, 2003, 09:21:18 ; Search time 4 Seconds

(without alignments)  
4.181 Million cell updates/sec

Title: A81835

Perfect score: 2787

Sequence: 1 ATGAAGTCTTCTTCCCAA.....GAGCAAAATACCAATCTAA 2787

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 3000 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : us-09-428-122-1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2775.8	99.6	3000	1	us-09-428-122-1

## ALIGNMENTS

RESULT 1					
us-09-428-122-1					
Query Match 99.6%; Score 2775.8; DB 1; Length 3000;					
Best Local Similarity 99.7%; Pred. No. 0;					
Matches 2780; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
Qy	1	ATGAAGTCTTCTTCCCAAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTCTGCTATG	60		
Db	101	ATGAAGTCTTCTTCCCAAAGTTTGTATTTCTACATTTGCTATTTTCCCTTTCTGCTATG	160		
Qy	61	ATTGCTACCGAGACAGTTTGGATTCAAGTGGCGATTTTCGATGGGAATAAAATGGTAAT	120		
Db	161	ATTGCTACCGAGACAGTTTGGATTCAAGTGGCGATTTTCGATGGGAATAAAATGGTAAT	220		
Qy	121	TTTTCAGTTTCTGAGAGTTCAGGAAGATGCTGGAATCTTACTTCTATTTTAAAGGGAATGTC	180		
Db	221	TTTTCAGTTTCTGAGAGTTCAGGAAGATGCTGGAATCTTACTTCTATTTTAAAGGGAATGTC	280		
Qy	181	ACTCTAGAAATATTCCTGGAACAGCAAGCAATCAAAAGCTGTTTAAACAACACT	240		
Db	281	ACTCTAGAAATATTCCTGGAACAGCAAGCAATCAAAAGCTGTTTAAACAACACT	340		
Qy	241	AAGGGGATTTGACTTTCACAGTACCGGAACTCTATTTGTTCCAAACGGTGGATGCA	300		
Db	341	AAGGGGATTTGACTTTCACAGTACCGGAACTCTATTTGTTCCAAACGGTGGATGCA	400		

Qy	301	GGGACTGTAGCAGCGGCTGCTGTATTAACAGCAGCGCTGTAGATAAAATCTACACGTTTATA	360		
Db	401	GGGACTGTAGCAGCGGCTGCTGTATTAACAGCAGCGCTGTAGATAAAATCTACACGTTTATA	460		
Qy	361	GGGTTTCTTCGCTATCTTTTATTTGCTCTCCCTGGAGTTTCGATAACTACCGGCAAGA	420		
Db	461	GGGTTTCTTCGCTATCTTTTATTTGCTCTCCCTGGAGTTTCGATAACTACCGGCAAGA	520		
Qy	421	GCCGTTAGCTCTCTACGGGTAGCTTCAAGTTTGCACAAAATCTCAGTTTGTCTTTCAGC	480		
Db	521	GCCGTTAGCTCTCTACGGGTAGCTTCAAGTTTGCACAAAATCTCAGTTTGTCTTTCAGC	580		
Qy	481	AAAACTTTTCAACGGATAATGGCGGTCTATCAACCGCAAAAATCTTTTCATTAACAGG	540		
Db	581	AAAACTTTTCAACGGATAATGGCGGTCTATCAACCGCAAAAATCTTTTCATTAACAGG	640		
Qy	541	ACTCAATGTCTAGCTCTGTTTCTGAAAATACCTCTCAAGAAAGCGGAGCATTCAG	600		
Db	641	ACTCAATGTCTAGCTCTGTTTCTGAAAATACCTCTCAAGAAAGCGGAGCATTCAG	700		
Qy	601	ACTTCOGATGCCCTTACCATTTCTGGAACCAAGGGGAAGTCTCTTTTCTGCAATACT	660		
Db	701	ACTTCOGATGCCCTTACCATTTCTGGAACCAAGGGGAAGTCTCTTTTCTGCAATACT	760		
Qy	661	TCTTCGGATTCCTGAGCTGCAATTTTTCACAGAGCCTCGGTGACTATTTCTATATATGCT	720		
Db	761	TCTTCGGATTCCTGAGCTGCAATTTTTCACAGAGCCTCGGTGACTATTTCTATATATGCT	820		
Qy	721	AAAGTTTCTTTTATTGACAAATAGGTCAAGGAGCGAGCTCTCTCAACAGCGGGGATATG	780		
Db	821	AAAGTTTCTTTTATTGACAAATAGGTCAAGGAGCGAGCTCTCTCAACAGCGGGGATATG	880		
Qy	781	TCAGAGGTGCTATCTGCTTATTAACCTAGTACAGATTAAGCTCACTCCCTCACTGGA	840		
Db	881	TCAGAGGTGCTATCTGCTTATTAACCTAGTACAGATTAAGCTCACTCCCTCACTGGA	940		
Qy	841	AATCAGATGTTTACTCTTCAGCAACATATCATCTGACAAACAGCGGGAGGAGCTATATG	900		
Db	941	AATCAGATGTTTACTCTTCAGCAACATATCATCTGACAAACAGCGGGAGGAGCTATATG	1000		
Qy	901	AAAAAGCTCGAACTGGCTTCGGAGGAGCTTACCTATTCAGTAAATAGTGTCAATGGA	960		
Db	1001	AAAAAGCTCGAACTGGCTTCGGAGGAGCTTACCTATTCAGTAAATAGTGTCAATGGA	1060		
Qy	961	GGTACAGCTCTTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCC	1020		
Db	1061	GGTACAGCTCTTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCC	1120		
Qy	1021	GCCGATAGTGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTGGGAGC	1080		
Db	1121	GCCGATAGTGTGACATTTCTTTTATAGGAATACAGTCACTTCTACTCTCTGGGAGC	1180		
Qy	1081	AATAGAAGTATGATCGACTTAGGAAACGAGTGCAGGATGACAGCTTTCGCTGCTGCT	1140		
Db	1181	AATAGAAGTATGATCGACTTAGGAAACGAGTGCAGGATGACAGCTTTCGCTGCTGCT	1240		
Qy	1141	GGTAGAGCCATCTACTTATGATCCCATAACTACAGATCTTCCCAACAGTTACAGAT	1200		
Db	1241	GGTAGAGCCATCTACTTATGATCCCATAACTACAGATCTTCCCAACAGTTACAGAT	1300		
Qy	1201	GTCTTAAAGTTAATGAGCTTCGGCAGATTTCTGCACTACAATATACAGGAAACATCATC	1260		
Db	1301	GTCTTAAAGTTAATGAGCTTCGGCAGATTTCTGCACTACAATATACAGGAAACATCATC	1360		
Qy	1261	TTTCAAGAGAAAATGTTATACAGACAGAGCGCGCAGATTCTTAAATCTTACTTCGAAG	1320		
Db	1361	TTTCAAGAGAAAATGTTATACAGACAGAGCGCGCAGATTCTTAAATCTTACTTCGAAG	1420		
Qy	1321	CTACTACAGCCTGTAACTCTTTTACAGAGGTACTCTTCTTAAACATGAGGTGACTCTG	1380		
Db	1421	CTACTACAGCCTGTAACTCTTTTACAGAGGTACTCTTCTTAAACATGAGGTGACTCTG	1480		
Qy	1381	CAGACTCAGGCATTTCACTCAACAGCGAGATTTCTGCTCGAAATGGACGTAGGAACACT	1440		

1481 CAGACTCAGGCAATTCACCTCAACAGGCGAGTTCTCGCTCGAATGGACGTAGGAATCA 1540  
1441 CTAGAACCTGCTGATACCTAGCAACATTAACAAATTTGGTCAATTAACATCAGTTCTATAGAC 1500  
1541 CTAGAACCTGCTGATACCTAGCAACATTAACAAATTTGGTCAATTAACATCAGTTCTATAGAC 1600  
1501 GZTGCAGAGGAGGCAAAATTAAGAACCAAGCTAGCTCAAAATTCGACTTTATCTGGA 1560  
1601 GZTGCAGAGGAGGCAAAATTAAGAACCAAGCTAGCTCAAAATTCGACTTTATCTGGA 1660  
1561 ACCATCACTTTATTTGAGACCCGACGCGGCACTTTATGAAAATCATAGTTTAAAGAAATCCT 1620  
1661 ACCATCACTTTATTTGAGACCCGACGCGGCACTTTATGAAAATCATAGTTTAAAGAAATCCT 1720  
1621 CAGTCTCAGCACTCTTAGAGCTCAAAAGCTTTCTGAACTGTAAACAGCACCCGAGTACT 1680  
1721 CAGTCTCAGCACTCTTAGAGCTCAAAAGCTTTCTGAACTGTAAACAGCACCCGAGTACT 1780  
1681 CCAGATCTCTTAATGGGTGAGAAATTCATTAAGCTATCAGGGAACCTTGGGGCCCAATT 1740  
1781 CCAGATCTCTTAATGGGTGAGAAATTCATTAAGCTATCAGGGAACCTTGGGGCCCAATT 1840  
1741 GTTTCGGGACAGGCGGCTTCTACGACTGCAACCTTCAACTGGACTAAATCTGCTATATT 1800  
1841 GTTTCGGGACAGGCGGCTTCTACGACTGCAACCTTCAACTGGACTAAATCTGCTATATT 1900  
1801 CCTAATCCGAGCGTATCGGCTCTTATGCTGCTTAATAGCTTATGAACTGCAATTTATAGAT 1860  
1901 CCTAATCCGAGCGTATCGGCTCTTATGCTGCTTAATAGCTTATGAACTGCAATTTATAGAT 1960  
1861 ATTAGCTCTCTCCATTAATTTATGAGACTGCAACGAGGTTGAGGAGACCCGTGCT 1920  
1961 ATTAGCTCTCTCCATTAATTTATGAGACTGCAACGAGGTTGAGGAGACCCGTGCT 2020  
1921 TTTTGGTGTCTGAGTATTAATCTTCTTCCATAGGATAGTAAACAGGAGGTTGAGGAGACCCGTGCT 1980  
2021 TTTTGGTGTCTGAGTATTAATCTTCTTCCATAGGATAGTAAACAGGAGGTTGAGGAGACCCGTGCT 2080  
1981 TTTTCGCCATTTGAGTGGGCGGTTATGTCATAGGAGGAAACCTTATCTGTTTCAGATAAG 2040  
2081 TTTTCGCCATTTGAGTGGGCGGTTATGTCATAGGAGGAAACCTTATCTGTTTCAGATAAG 2140  
2041 ATTCTTAGTGTCTGCTATTTGTCAGCTCTTTTGGAGAGATAGAGACTTCTTGTAGCTAAG 2100  
2141 ATTCTTAGTGTCTGCTATTTGTCAGCTCTTTTGGAGAGATAGAGACTTCTTGTAGCTAAG 2200  
2101 AATCAGGTACAGTCTACGAGGAACTCTTATTAACGAGCAAGAAACCTTATCTCT 2160  
2201 AATCAGGTACAGTCTACGAGGAACTCTTATTAACGAGCAAGAAACCTTATCTCT 2260  
2161 CTTCTTGTCAAACTACGCGCTTGTGTTGCTTATGTTCTTACAGAGATTCCTGTTCTC 2220  
2261 CTTCTTGTCAAACTACGCGCTTGTGTTGCTTATGTTCTTACAGAGATTCCTGTTCTC 2320  
2221 TTTTCAGGAAACCTTAGCTTACACCCATACGATACCTTGAAGAAACCAAGTATACACA 2280  
2321 TTTTCAGGAAACCTTAGCTTACACCCATACGATACCTTGAAGAAACCAAGTATACACA 2380  
2281 TATCTTACTGTTTAAAGGAGCTGGGGGAAATGATAGTTTGGCTTTAGAAATTCGGTGGAGA 2340  
2381 TATCTTACTGTTTAAAGGAGCTGGGGGAAATGATAGTTTGGCTTTAGAAATTCGGTGGAGA 2440  
2341 GCTCCGATTTGCTTATGATGAAAGTGTCTTATTTAGAGAGTACATGCTTTCATGAAATTG 2400  
2441 GCTCCGATTTGCTTATGATGAAAGTGTCTTATTTAGAGAGTACATGCTTTCATGAAATTG 2500  
2401 CAGTTTGTCTATGCACTCAGGAGGTTTAAAGAAACAGGGAACAGAGCTCTGTAATT 2460  
2501 CAGTTTGTCTATGCACTCAGGAGGTTTAAAGAAACAGGGAACAGAGCTCTGTAATT 2560  
2461 GGAAGTAGCCGCTCTTGTGATCTTGTCTTATCTTACCTATCGGATCCGATTTGATAGGAATCA 2520

2561 GGAAGTAGCCGCTCTTGTGAAATCTTGCCTTACCTATCGGATCCGATTTGATAGGAATCA 2620  
2521 GACTGCCAAGATGCAACGTACCAATCTTAATCTTGGTTATCTGTTGGATCTTGTTCGTAGT 2580  
2621 GACTGCCAAGATGCAACGTACCAATCTTAATCTTGGTTATCTGTTGGATCTTGTTCGTAGT 2680  
2581 AACCCGACTGTACGACCAACACTGCGAATTTAGCGGTGATCTTGGAAACCTTCGGTACG 2640  
2681 AACCCGACTGTACGACCAACACTGCGAATTTAGCGGTGATCTTGGAAACCTTCGGTACG 2740  
2641 AATTGGCAAGACAGCTTTAGTCTTCTGTCGAGGAAACCAATTTTGTCTTAACTCAAT 2700  
2741 AATTGGCAAGACAGCTTTAGTCTTCTGTCGAGGAAACCAATTTTGTCTTAACTCAAT 2800  
2701 TTTGAAGCCTTTAGCCCAATTTCTTTTGAATTTGCTGGGTCACTCGCAATTTACAATGTA 2760  
2801 TTTGAAGCCTTTAGCCCAATTTCTTTTGAATTTGCTGGGTCACTCGCAATTTACAATGTA 2860  
2761 GACTTAGAGGCAAAATACCAATTTCTAA 2787  
2861 GACTTAGAGGCAAAATACCAATTTCTAA 2887

Search completed: December 3, 2003, 09:21:23  
Job time : 4 secs